

RAW SEQUENCE LISTING

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Application Serial Number: 10/810,486
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/810,486

DATE: 11/18/2004
TIME: 16:44:53

Input Set : D:\401c1.app.txt
Output Set: N:\CRF4\11182004\J810486.raw

3 <110> APPLICANT: Furusawa, Mitsuru
6 <120> TITLE OF INVENTION: METHOD AND SYSTEM FOR RAPIDLY CONFERRING
7 A DESIRED TRAIT TO AN ORGANISM
9 <130> FILE REFERENCE: 690116.401C1
11 <140> CURRENT APPLICATION NUMBER: 10/810,486
12 <141> CURRENT FILING DATE: 2004-03-26
14 <150> PRIOR APPLICATION NUMBER: US 10/684,141
15 <151> PRIOR FILING DATE: 2003-10-10
17 <150> PRIOR APPLICATION NUMBER: JP 2003-092898
18 <151> PRIOR FILING DATE: 2003-03-28
20 <160> NUMBER OF SEQ ID NOS: 95
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3551
26 <212> TYPE: DNA
27 <213> ORGANISM: *Saccharomyces cerevisiae*
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32 gagcacttgc tattaaagcat taatctttat acatatacgc acagcaatga gtgaaaaaaag 180
33 atcccttccc atgggtttagt tgaagatcga tgacgaggat actccccagt tggaaaagaa 240
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38 ttttgaccca agttttagt atatttctt ccaacaaatt gatgcggAAC agaggctact 540
39 gaatggtatac aaagatgaaa atacatctac cgtggtaagg ttttttggtg tcactagtga 600
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41 caattcttcc gacgctaacg atcaggagca aatcaacaag tttgtgcact atttaaacga 720
42 aacatttgac cacgctattt attcgtattt aatgttatct aacacgtcta tctgggtta 780
43 ttccggagat accaaattac cattctggaa aatatacgtc acctatccgc atatggtaa 840
44 caaactgcgt actgcgtttg aaagaggtca tctttcattt aactcgttgt tttctaacgg 900
45 cacgactact tatgataaca ttgcctacac tttaaggta atggtagatt gtggaaattgt 960
46 cggtatgtcc tggataacat taccaaaagg aaagtattcg atgattgagc ctaataacag 1020
47 agttccctt tgcagggttgg aagtttcaat taattatgt aacctaatacg cacatcctgc 1080
48 tgagggtgat tggtctcata cagctccatt gcgtatcatg tcctttgata tcgagtggtgc 1140
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 58 cgatagtgaa acaagaagaa gttggccgt ttactgttg aaagacgcct acctgccc 1740
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 60 tggccattt tcataattac tagctcggt tcaacaaatt aaagttgtt ctcaactatt 1860
 61 tcgaaagtgc ctggagattg atactgtgat acctaacatg caatctcagg cctctgatga 1920
 62 ccaatatgag ggtgcactg ttattgagcc tattcgttgt tattacgatg taccgattgc 1980
 63 aactttggat ttcaattctt tatataccaag tattatgatg gcgcacaacc tatgttatac 2040
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 66 tattctggat gaattaataa gtgctagaaa acgcgcctaa aaagatctga gagatgagaa 2220
 67 ggatccattt aaaaagagatg ttttaatgg tagacaattt gctttaaaga tttagctaa 2280
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 82 gaaatccatt aaaaatttaca caggctctca aaaaggaggc ttgtatgagct ttataaaaaa 3180
 83 agttgaggct tggaaaagtt gtaaagggtcc gttgaggaaa ggtgaaggcc ctctttgttc 3240
 84 aaactgtcta gcaaggctcg gagaattata cataaaggca ttatacgatg tcagagattt 3300
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 86 tgaagttttg tggcaataa agaactgtga catttttat atgcgggtta aggtaaaaaa 3420
 87 agagctgcag gagaagatg aacaattaag caaatggtaa aaaacgatag ggtggcacat 3480
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 89 taaatagata c 3551
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 93 <211> LENGTH: 1097
 94 <212> TYPE: PRT
 95 <213> ORGANISM: *Saccharomyces cerevisiae*
 97 <400> SEQUENCE: 2
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 99 1 5 10 15
 100 Glu Asp Thr Pro Gln Leu Glu Lys Lys Ile Lys Arg Gln Ser Ile Asp
 101 20 25 30
 102 His Gly Val Gly Ser Glu Pro Val Ser Thr Ile Glu Ile Ile Pro Ser
 103 35 40 45
 104 Asp Ser Phe Arg Lys Tyr Asn Ser Gln Gly Phe Lys Ala Lys Asp Thr
 105 50 55 60
 106 Asp Leu Met Gly Thr Gln Leu Glu Ser Thr Phe Glu Gln Glu Leu Ser
 107 65 70 75 80

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109 85 90 95
110 Phe Glu Arg Lys Lys Leu Pro Thr Asp Phe Asp Pro Ser Leu Tyr Asp
111 100 105 110
112 Ile Ser Phe Gln Gln Ile Asp Ala Glu Gln Ser Val Leu Asn Gly Ile
113 115 120 125
114 Lys Asp Glu Asn Thr Ser Thr Val Val Arg Phe Phe Gly Val Thr Ser
115 130 135 140
116 Glu Gly His Ser Val Leu Cys Asn Val Thr Gly Phe Lys Asn Tyr Leu
117 145 150 155 160
118 Tyr Val Pro Ala Pro Asn Ser Ser Asp Ala Asn Asp Gln Glu Gln Ile
119 165 170 175
120 Asn Lys Phe Val His Tyr Leu Asn Glu Thr Phe Asp His Ala Ile Asp
121 180 185 190
122 Ser Ile Glu Val Val Ser Lys Gln Ser Ile Trp Gly Tyr Ser Gly Asp
123 195 200 205
124 Thr Lys Leu Pro Phe Trp Lys Ile Tyr Val Thr Tyr Pro His Met Val
125 210 215 220
126 Asn Lys Leu Arg Thr Ala Phe Glu Arg Gly His Leu Ser Phe Asn Ser
127 225 230 235 240
128 Trp Phe Ser Asn Gly Thr Thr Tyr Asp Asn Ile Ala Tyr Thr Leu
129 245 250 255
130 Arg Leu Met Val Asp Cys Gly Ile Val Gly Met Ser Trp Ile Thr Leu
131 260 265 270
132 Pro Lys Gly Lys Tyr Ser Met Ile Glu Pro Asn Asn Arg Val Ser Ser
133 275 280 285
134 Cys Gln Leu Glu Val Ser Ile Asn Tyr Arg Asn Leu Ile Ala His Pro
135 290 295 300
136 Ala Glu Gly Asp Trp Ser His Thr Ala Pro Leu Arg Ile Met Ser Phe
137 305 310 315 320
138 Asp Ile Glu Cys Ala Gly Arg Ile Gly Val Phe Pro Glu Pro Glu Tyr
139 325 330 335
140 Asp Pro Val Ile Gln Ile Ala Asn Val Val Ser Ile Ala Gly Ala Lys
141 340 345 350
142 Lys Pro Phe Ile Arg Asn Val Phe Thr Leu Asn Thr Cys Ser Pro Ile
143 355 360 365
144 Thr Gly Ser Met Ile Phe Ser His Ala Thr Glu Glu Met Leu Ser
145 370 375 380
146 Asn Trp Arg Asn Phe Ile Ile Lys Val Asp Pro Asp Val Ile Ile Gly
147 385 390 395 400
148 Tyr Asn Thr Thr Asn Phe Asp Ile Pro Tyr Leu Leu Asn Arg Ala Lys
149 405 410 415
150 Ala Leu Lys Val Asn Asp Phe Pro Tyr Phe Gly Arg Leu Lys Thr Val
151 420 425 430
152 Lys Gln Glu Ile Lys Glu Ser Val Phe Ser Ser Lys Ala Tyr Gly Thr
153 435 440 445
154 Arg Glu Thr Lys Asn Val Asn Ile Asp Gly Arg Leu Gln Leu Asp Leu
155 450 455 460
156 Leu Gln Phe Ile Gln Arg Glu Tyr Lys Leu Arg Ser Tyr Thr Leu Asn

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160	Ser	Ile	Ile	Ser	Asp	Leu	Gln	Asn	Gly	Asp	Ser	Glu	Thr	Arg	Arg	Arg
161																510
162	Leu	Ala	Val	Tyr	Cys	Leu	Lys	Asp	Ala	Tyr	Leu	Pro	Leu	Arg	Leu	Met
163																525
164	Glu	Lys	Leu	Met	Ala	Leu	Val	Asn	Tyr	Thr	Glu	Met	Ala	Arg	Val	Thr
165																540
166	Gly	Val	Pro	Phe	Ser	Tyr	Leu	Leu	Ala	Arg	Gly	Gln	Gln	Ile	Lys	Val
167																560
168	Val	Ser	Gln	Leu	Phe	Arg	Lys	Cys	Leu	Glu	Ile	Asp	Thr	Val	Ile	Pro
169																575
170	Asn	Met	Gln	Ser	Gln	Ala	Ser	Asp	Asp	Gln	Tyr	Glu	Gly	Ala	Thr	Val
171																590
172	Ile	Glu	Pro	Ile	Arg	Gly	Tyr	Tyr	Asp	Val	Pro	Ile	Ala	Thr	Leu	Asp
173																605
174	Phe	Asn	Ser	Leu	Tyr	Pro	Ser	Ile	Met	Met	Ala	His	Asn	Leu	Cys	Tyr
175																620
176	Thr	Thr	Leu	Cys	Asn	Lys	Ala	Thr	Val	Glu	Arg	Leu	Asn	Leu	Lys	Ile
177																640
178	Asp	Glu	Asp	Tyr	Val	Ile	Thr	Pro	Asn	Gly	Asp	Tyr	Phe	Val	Thr	Thr
179																655
180	Lys	Arg	Arg	Arg	Gly	Ile	Leu	Pro	Ile	Ile	Leu	Asp	Glu	Leu	Ile	Ser
181																670
182	Ala	Arg	Lys	Arg	Ala	Lys	Lys	Asp	Leu	Arg	Asp	Glu	Lys	Asp	Pro	Phe
183																685
184	Lys	Arg	Asp	Val	Leu	Asn	Gly	Arg	Gln	Leu	Ala	Leu	Lys	Ile	Ser	Ala
185																700
186	Asn	Ser	Val	Tyr	Gly	Phe	Thr	Gly	Ala	Thr	Val	Gly	Lys	Leu	Pro	Cys
187																720
188	Leu	Ala	Ile	Ser	Ser	Val	Thr	Ala	Tyr	Gly	Arg	Thr	Met	Ile	Leu	
189																735
190	Lys	Thr	Lys	Thr	Ala	Val	Gln	Glu	Lys	Tyr	Cys	Ile	Lys	Asn	Gly	Tyr
191																750
192	Lys	His	Asp	Ala	Val	Val	Val	Tyr	Gly	Asp	Thr	Asp	Ser	Val	Met	Val
193																765
194	Lys	Phe	Gly	Thr	Thr	Asp	Leu	Lys	Glu	Ala	Met	Asp	Leu	Gly	Thr	Glu
195																780
196	Ala	Ala	Lys	Tyr	Val	Ser	Thr	Leu	Phe	Lys	His	Pro	Ile	Asn	Leu	Glu
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198	Phe	Glu	Lys	Ala	Tyr	Phe	Pro	Tyr	Leu	Leu	Ile	Asn	Lys	Lys	Arg	Tyr
199																815
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202	Lys	Gly	Leu	Ala	Ser	Val	Arg	Arg	Asp	Ser	Cys	Ser	Leu	Val	Ser	Ile
203																845
204	Val	Met	Asn	Lys	Val	Leu	Lys	Lys	Ile	Leu	Ile	Glu	Arg	Asn	Val	Asp
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207 865 870 875 880
208 Arg Val Asp Ile Ser Lys Leu Ile Ile Ser Lys Thr Leu Ala Pro Asn
209 885 890 895
210 Tyr Thr Asn Pro Gln Pro His Ala Val Leu Ala Glu Arg Met Lys Arg
211 900 905 910
212 Arg Glu Gly Val Gly Pro Asn Val Gly Asp Arg Val Asp Tyr Val Ile
213 915 920 925
214 Ile Gly Gly Asn Asp Lys Leu Tyr Asn Arg Ala Glu Asp Pro Leu Phe
215 930 935 940
216 Val Leu Glu Asn Asn Ile Gln Val Asp Ser Arg Tyr Tyr Leu Thr Asn
217 945 950 955 960
218 Gln Leu Gln Asn Pro Ile Ile Ser Ile Val Ala Pro Ile Ile Gly Asp
219 965 970 975
220 Lys Gln Ala Asn Gly Met Phe Val Val Lys Ser Ile Lys Ile Asn Thr
221 980 985 990
222 Gly Ser Gln Lys Gly Gly Leu Met Ser Phe Ile Lys Lys Val Glu Ala
223 995 1000 1005
224 Cys Lys Ser Cys Lys Gly Pro Leu Arg Lys Gly Glu Gly Pro Leu Cys
225 1010 1015 1020
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227 1025 1030 1035 1040
228 Asp Val Arg Asp Leu Glu Glu Lys Tyr Ser Arg Leu Trp Thr Gln Cys
229 1045 1050 1055
230 Gln Arg Cys Ala Gly Asn Leu His Ser Glu Val Leu Cys Ser Asn Lys
231 1060 1065 1070
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239 <211> LENGTH: 7505
240 <212> TYPE: DNA
241 <213> ORGANISM: Saccharomyces cerevisiae
243 <400> SEQUENCE: 3
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256 gatgacatcg attcgatgat gggatttggaa agatacgatc cgccgcaata caatggcagg 780
257 tttgatgcga aggatataaga tcagattcca ggccgcgtag ggtggctgac gaacatgcac 840

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